



#4

1

SEQUENCE LISTING

<110> GEORGE, LISLE W
ANGELOS, JOHN A
HESS, JOHN F

<120> MORAXELLA BOVIS CYTOTOXIN, CYTOTOXIN GENE, ANTIBODIES
AND VACCINES FOR PREVENTION AND TREATMENT OF MORAXELLA
BOVIS INFECTIONS

<130> 481.06

<140> 09/884,696

<141> 2001-06-19

<160> 41

<170> PatentIn Ver. 2.1

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Gln	Thr	Gly	Ile	Ala	Ile	Ser	Ala	Thr	Lys	Leu	Glu	Lys	Phe	Leu	Gln	
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Ala Lys Gly Phe Ser Asn Ile Gly Asn Lys Leu Gln Asn Leu Asn Phe	
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Ser Lys Thr Asn Leu Gly Leu Glu Ile Ile Thr Gly Leu Leu Ser Gly	
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Phe Glu Asp Gly Lys Lys Val Glu Ala Gly Ser Asn Ile Thr Leu Asp	
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Ile Phe Val Gly Gln Gly Lys Met Asn Ile Asp Gly Gly Asp Gly His	
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Gly Ala Gly Asp Asp Arg Leu Phe Gly Gly Lys Gly Asn Asp Arg Leu	
725 730 735	
tct gga gat gaa ggc gat gat tta ctc gat ggc ggt tct ggt gat gat	2256
Ser Gly Asp Glu Gly Asp Asp Leu Leu Asp Gly Gly Ser Gly Asp Asp	
740 745 750	
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Val Leu Asn Gly Gly Ala Gly Asn Asp Val Tyr Ile Phe Arg Lys Gly	
755 760 765	
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Asp Gly Asn Asp Thr Leu Tyr Asp Gly Thr Gly Asn Asp Lys Leu Ala	
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 Phe Ala Asp Ala Asn Ile Ser Asp Ile Met Ile Glu Arg Thr Lys Glu
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ggc att ata gtt aaa cga aat gat cat tca ggc agt att aac ata cca 2448
 Gly Ile Ile Val Lys Arg Asn Asp His Ser Gly Ser Ile Asn Ile Pro
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aga tgg tac ata aca tca aat tta caa aat tat caa agt aat aaa aca 2496
 Arg Trp Tyr Ile Thr Ser Asn Leu Gln Asn Tyr Gln Ser Asn Lys Thr
 820 825 830

gat cat aaa att gag caa cta att ggc aaa gat ggc agt tat atc act 2544
 Asp His Lys Ile Glu Gln Leu Ile Gly Lys Asp Gly Ser Tyr Ile Thr
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tcc gat caa att gat aaa att ttg caa gat aag aaa gat ggc aca gta 2592
 Ser Asp Gln Ile Asp Lys Ile Leu Gln Asp Lys Lys Asp Gly Thr Val
 850 855 860

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 865 870 875 880

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 900 905 910

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Tyr Asp Pro Gln Lys Gly Gly Thr Leu Asn Asp Phe Ile Lys Ala Ala
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Asp Glu Leu Gly Ile Ala Arg Leu Ala Glu Glu Pro Asn His Thr Glu
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Thr Ala Lys Lys Ser Val Asp Thr Val Asn Gln Phe Leu Ser Leu Thr
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Ile	Asp	Arg	Lys	Leu	Gly	Lys	Ala	Ser	Asn	Val	Leu	Ser	Thr	Leu	Ser	115	120	125
Ser	Phe	Leu	Gly	Thr	Ala	Leu	Ala	Gly	Ile	Glu	Leu	Asp	Ser	Leu	Ile	130	135	140
Lys	Lys	Gly	Asp	Ala	Ala	Pro	Asp	Ala	Leu	Ala	Lys	Ala	Ser	Ile	Asp	145	150	155
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Glu	Ala	Phe	Ser	Ser	Gln	Leu	Ala	Lys	Leu	Gly	Ser	Thr	Ile	Ser	Gln	180	185	190
Ala	Lys	Gly	Phe	Ser	Asn	Ile	Gly	Asn	Lys	Leu	Gln	Asn	Leu	Asn	Phe	195	200	205
Ser	Lys	Thr	Asn	Leu	Gly	Leu	Glu	Ile	Ile	Thr	Gly	Leu	Leu	Ser	Gly	210	215	220
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His	Ala	Asn	Ala	Leu	Asp	Glu	Phe	Ala	Lys	Gln	Phe	Arg	Lys	Phe	Gly	305	310	315
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Ile	Glu	Ala	Ser	Leu	Thr	Thr	Ile	Ser	Thr	Ala	Leu	Gly	Ala	Val	Ser	340	345	350
Ala	Gly	Val	Ser	Ala	Ala	Ala	Val	Gly	Ser	Ala	Val	Gly	Ala	Pro	Ile	355	360	365
Ala	Leu	Leu	Val	Ala	Gly	Val	Thr	Gly	Leu	Ile	Ser	Gly	Ile	Leu	Glu	370	375	380

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Lys	Gly	Tyr	Asp	Ser	Arg	Tyr	Ala	Ala	Tyr	Leu	Ala	Asn	Asn	Leu	Lys	420	425	430	
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Lys	Leu	Asp	Phe	Ser	Lys	Val	Ile	Gln	Arg	Val	Ala	Glu	Thr	Glu	Gly	565	570	575	
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Ile	Phe	Val	Gly	Gln	Gly	Lys	Met	Asn	Ile	Asp	Gly	Gly	Asp	Gly	His	595	600	605	
Asp	Arg	Val	Phe	Tyr	Ser	Lys	Asp	Gly	Gly	Phe	Gly	Asn	Ile	Thr	Val	610	615	620	
Asp	Gly	Thr	Ser	Ala	Thr	Glu	Ala	Gly	Ser	Tyr	Thr	Val	Asn	Arg	Lys	625	630	635	640
Val	Ala	Arg	Gly	Asp	Ile	Tyr	His	Glu	Val	Val	Lys	Arg	Gln	Glu	Thr	645	650	655	
Lys	Val	Gly	Lys	Arg	Thr	Glu	Thr	Ile	Gln	Tyr	Arg	Asp	Tyr	Glu	Leu	660	665	670	
Arg	Lys	Val	Gly	Tyr	Gly	Tyr	Gln	Ser	Thr	Asp	Asn	Leu	Lys	Ser	Val	675	680	685	

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 Gly Ala Gly Asp Asp Arg Leu Phe Gly Gly Lys Gly Asn Asp Arg Leu
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 Ser Gly Asp Glu Gly Asp Asp Leu Leu Asp Gly Gly Ser Gly Asp Asp
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 Val Leu Asn Gly Gly Ala Gly Asn Asp Val Tyr Ile Phe Arg Lys Gly
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 Pro Gln Asn Tyr Gln Tyr Asp Thr Glu Gln Gly Asn Gly Leu Gln Asp
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 Leu Val Lys Ala Ala Glu Leu Gly Ile Glu Val Gln Arg Glu Glu
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 Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu Gly Thr Ile Gln Thr
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 Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu Ser Ala Pro Gln Ile
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 Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys Thr Val Leu Ser Gly
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 Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala Asn Gln Val Val Gly
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 Thr Glu Ile Asp Gly Gly Glu Gly Tyr Asp Arg Val His Tyr Ser Arg
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Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr Lys Glu Thr Glu Gln
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 Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser Asn Leu Lys Asp Leu
 805 810 815
 Thr Phe Glu Lys Val Lys His Asn Leu Val Ile Thr Asn Ser Lys Lys
 820 825 830
 Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu Ala Asp Phe Ala Lys
 835 840 845
 Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu Lys Ile Glu Glu Ile
 850 855 860
 Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys Gln Val Asp Asp Leu
 865 870 875 880
 Ile Ala Lys Gly Asn Gly Lys Ile Thr Gln Asp Glu Leu Ser Lys Val
 885 890 895
 Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys Asn Val Thr Asn Ser
 900 905 910
 Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe Thr Ser Ser Asn Asp
 915 920 925
 Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met Leu Asp Gln Ser Leu
 930 935 940

Ser Ser Leu Gln Phe Ala Arg Ala Ala
945 950

<210> 4

<211> 956

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 4

Met Ser Lys Ile Thr Leu Ser Ser Leu Lys Ser Ser Leu Gln Gln Gly
1 5 10 15

Leu Lys Asn Gly Lys Asn Lys Leu Asn Gln Ala Gly Thr Thr Leu Lys
20 25 30

Asn Gly Leu Thr Gln Thr Gly His Ser Leu Gln Asn Gly Ala Lys Lys
35 40 45

Leu Ile Leu Tyr Ile Pro Gln Gly Tyr Asp Ser Gly Gln Gly Asn Gly
50 55 60

Val Gln Asp Leu Val Lys Ala Ala Asn Asp Leu Gly Ile Glu Val Trp
65 70 75 80

Arg Glu Glu Arg Ser Asn Leu Asp Ile Ala Lys Thr Ser Phe Asp Thr
85 90 95

Thr Gln Lys Ile Leu Gly Phe Thr Asp Arg Gly Ile Val Leu Phe Ala
100 105 110

Pro Gln Leu Asp Asn Leu Leu Lys Lys Asn Pro Lys Ile Gly Asn Thr
115 120 125

Leu Gly Ser Ala Ser Ser Ile Ser Gln Asn Ile Gly Lys Ala Asn Thr
130 135 140

Val Leu Gly Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ser Gly Val
145 150 155 160

Asn Leu Asn Glu Leu Leu Gln Asn Lys Asp Pro Asn Gln Leu Glu Leu
165 170 175

Ala Lys Ala Gly Leu Glu Leu Thr Asn Glu Leu Val Gly Asn Ile Ala
180 185 190

Ser Ser Val Gln Thr Val Asp Ala Phe Ala Glu Gln Ile Ser Lys Leu
195 200 205

Gly Ser His Leu Gln Asn Val Lys Gly Leu Gly Gly Leu Ser Asn Lys
210 215 220

Leu Gln Asn Leu Pro Asp Leu Gly Lys Ala Ser Leu Gly Leu Asp Ile
225 230 235 240

Ile Ser Gly Leu Leu Ser Gly Ala Ser Ala Gly Leu Ile Leu Ala Asp
245 250 255

Lys	Glu	Ala	Ser	Thr	Glu	Lys	Lys	Ala	Ala	Ala	Gly	Val	Glu	Phe	Ala	
			260					265					270			
Asn	Gln	Ile	Ile	Gly	Asn	Val	Thr	Lys	Ala	Val	Ser	Ser	Tyr	Ile	Leu	
		275					280					285				
Ala	Gln	Arg	Val	Ala	Ser	Gly	Leu	Ser	Ser	Thr	Gly	Pro	Val	Ala	Ala	
	290					295					300					
Leu	Ile	Ala	Ser	Thr	Val	Ala	Leu	Ala	Val	Ser	Pro	Leu	Ser	Phe	Leu	
305					310					315					320	
Asn	Val	Ala	Asp	Lys	Phe	Lys	Gln	Ala	Asp	Leu	Ile	Lys	Ser	Tyr	Ser	
				325					330					335		
Glu	Arg	Phe	Gln	Lys	Leu	Gly	Tyr	Asp	Gly	Asp	Arg	Leu	Leu	Ala	Asp	
			340					345					350			
Phe	His	Arg	Glu	Thr	Gly	Thr	Ile	Asp	Ala	Ser	Val	Thr	Thr	Ile	Asn	
		355					360						365			
Thr	Ala	Leu	Ala	Ala	Ile	Ser	Gly	Gly	Val	Gly	Ala	Ala	Ser	Ala	Gly	
	370					375					380					
Ser	Leu	Val	Gly	Ala	Pro	Val	Ala	Leu	Leu	Val	Ala	Gly	Val	Thr	Gly	
385					390					395					400	
Leu	Ile	Thr	Thr	Ile	Leu	Glu	Tyr	Ser	Lys	Gln	Ala	Met	Phe	Glu	His	
				405					410					415		
Val	Ala	Asn	Lys	Val	His	Asp	Arg	Ile	Val	Glu	Trp	Glu	Lys	Lys	His	
			420					425					430			
Asn	Lys	Asn	Tyr	Phe	Glu	Gln	Gly	Tyr	Asp	Ser	Arg	His	Leu	Ala	Asp	
		435					440					445				
Leu	Gln	Asp	Asn	Met	Lys	Phe	Leu	Ile	Asn	Leu	Asn	Lys	Glu	Leu	Gln	
	450					455					460					
Ala	Glu	Arg	Val	Val	Ala	Ile	Thr	Gln	Gln	Arg	Trp	Asp	Asn	Gln	Ile	
465					470					475					480	
Gly	Asp	Leu	Ala	Ala	Ile	Ser	Arg	Arg	Thr	Asp	Lys	Ile	Ser	Ser	Gly	
				485					490					495		
Lys	Ala	Tyr	Val	Asp	Ala	Phe	Glu	Glu	Gly	Gln	His	Gln	Ser	Tyr	Asp	
			500					505					510			
Ser	Ser	Val	Gln	Leu	Asp	Asn	Lys	Asn	Gly	Ile	Ile	Asn	Ile	Ser	Asn	
		515					520					525				
Thr	Asn	Arg	Lys	Thr	Gln	Ser	Val	Leu	Phe	Arg	Thr	Pro	Leu	Leu	Thr	
	530					535					540					
Pro	Gly	Glu	Glu	Asn	Arg	Glu	Arg	Ile	Gln	Glu	Gly	Lys	Asn	Ser	Tyr	
545					550					555					560	

Ile	Thr	Lys	Leu	His	Ile	Gln	Arg	Val	Asp	Ser	Trp	Thr	Val	Thr	Asp	
				565					570						575	
Gly	Asp	Ala	Ser	Ser	Ser	Val	Asp	Phe	Thr	Asn	Val	Val	Gln	Arg	Ile	
			580					585					590			
Ala	Val	Lys	Phe	Asp	Asp	Ala	Gly	Asn	Ile	Ile	Glu	Ser	Lys	Asp	Thr	
		595					600					605				
Lys	Ile	Ile	Ala	Asn	Leu	Gly	Ala	Gly	Asn	Asp	Asn	Val	Phe	Val	Gly	
	610					615					620					
Ser	Ser	Thr	Thr	Val	Ile	Asp	Gly	Gly	Asp	Gly	His	Asp	Arg	Val	His	
625					630					635					640	
Tyr	Ser	Arg	Gly	Glu	Tyr	Gly	Ala	Leu	Val	Ile	Asp	Ala	Thr	Ala	Glu	
				645					650					655		
Thr	Glu	Lys	Gly	Ser	Tyr	Ser	Val	Lys	Arg	Tyr	Val	Gly	Asp	Ser	Lys	
			660					665					670			
Ala	Leu	His	Glu	Thr	Ile	Ala	Thr	His	Gln	Thr	Asn	Val	Gly	Asn	Arg	
		675					680					685				
Glu	Glu	Lys	Ile	Glu	Tyr	Arg	Arg	Glu	Asp	Asp	Arg	Phe	His	Thr	Gly	
	690					695					700					
Tyr	Thr	Val	Thr	Asp	Ser	Leu	Lys	Ser	Val	Glu	Glu	Ile	Ile	Gly	Ser	
705					710					715					720	
Gln	Phe	Asn	Asp	Ile	Phe	Lys	Gly	Ser	Gln	Phe	Asp	Asp	Val	Phe	His	
				725					730					735		
Gly	Gly	Asn	Gly	Val	Asp	Thr	Ile	Asp	Gly	Asn	Asp	Gly	Asp	Asp	His	
			740					745					750			
Leu	Phe	Gly	Gly	Ala	Gly	Asp	Asp	Val	Ile	Asp	Gly	Gly	Asn	Gly	Asn	
		755					760					765				
Asn	Phe	Leu	Val	Gly	Gly	Thr	Gly	Asn	Asp	Ile	Ile	Ser	Gly	Gly	Lys	
	770					775					780					
Asp	Asn	Asp	Ile	Tyr	Val	His	Lys	Thr	Gly	Asp	Gly	Asn	Asp	Ser	Ile	
785					790					795					800	
Thr	Asp	Ser	Gly	Gly	Gln	Asp	Lys	Leu	Ala	Phe	Ser	Asp	Val	Asn	Leu	
				805					810					815		
Lys	Asp	Leu	Thr	Phe	Lys	Lys	Val	Asp	Ser	Ser	Leu	Glu	Ile	Ile	Asn	
			820					825					830			
Gln	Lys	Gly	Glu	Lys	Val	Arg	Ile	Gly	Asn	Trp	Phe	Leu	Glu	Asp	Asp	
		835					840					845				
Leu	Ala	Ser	Thr	Val	Ala	Asn	Tyr	Lys	Ala	Thr	Asn	Asp	Arg	Lys	Ile	
	850					855					860					

Glu Glu Ile Ile Gly Lys Gly Gly Glu Arg Ile Thr Ser Glu Gln Val
 865 870 875 880
 Asp Lys Leu Ile Lys Glu Gly Asn Asn Gln Ile Ser Ala Glu Ala Leu
 885 890 895
 Ser Lys Val Val Asn Asp Tyr Asn Thr Ser Lys Asp Arg Gln Asn Val
 900 905 910
 Ser Asn Ser Leu Ala Lys Leu Ile Ser Ser Val Gly Ser Phe Thr Ser
 915 920 925
 Ser Ser Asp Phe Arg Asn Asn Leu Gly Thr Tyr Val Pro Ser Ser Ile
 930 935 940
 Asp Val Ser Asn Asn Ile Gln Leu Ala Arg Ala Ala
 945 950 955

<210> 5
 <211> 1023
 <212> PRT
 <213> Escherichia coli

<400> 5
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 Asp Ala Leu Lys Lys Ala Ala Glu Gln Thr Arg Asn Ala Gly Asn Arg
 35 40 45
 Leu Ile Leu Leu Ile Pro Lys Asp Tyr Lys Gly Gln Gly Ser Ser Leu
 50 55 60
 Asn Asp Leu Val Arg Thr Ala Asp Glu Leu Gly Ile Glu Val Gln Tyr
 65 70 75 80
 Asp Glu Lys Asn Gly Thr Ala Ile Thr Lys Gln Val Phe Gly Thr Ala
 85 90 95
 Glu Lys Leu Ile Gly Leu Thr Glu Arg Gly Val Thr Ile Phe Ala Pro
 100 105 110
 Gln Leu Asp Lys Leu Leu Gln Lys Tyr Gln Lys Ala Gly Asn Lys Leu
 115 120 125
 Gly Gly Ser Ala Glu Asn Ile Gly Asp Asn Leu Gly Lys Ala Gly Ser
 130 135 140
 Val Leu Ser Thr Phe Gln Asn Phe Leu Gly Thr Ala Leu Ser Ser Met
 145 150 155 160
 Lys Ile Asp Glu Leu Ile Lys Lys Gln Lys Ser Gly Gly Asn Val Ser
 165 170 175

Ser Ser Glu Leu Ala Lys Ala Ser Ile Glu Leu Ile Asn Gln Leu Val
 180 185 190
 Asp Thr Ala Ala Ser Leu Asn Asn Val Asn Ser Phe Ser Gln Gln Leu
 195 200 205
 Asn Lys Leu Gly Ser Val Leu Ser Asn Thr Lys His Leu Asn Gly Val
 210 215 220
 Gly Asn Lys Leu Gln Asn Leu Pro Asn Leu Asp Asn Ile Gly Ala Gly
 225 230 235 240
 Leu Asp Thr Val Ser Gly Ile Leu Ser Ala Ile Ser Ala Ser Phe Ile
 245 250 255
 Leu Ser Asn Ala Asp Ala Asp Thr Gly Thr Lys Ala Ala Ala Gly Val
 260 265 270
 Glu Leu Thr Thr Lys Val Leu Gly Asn Val Gly Lys Gly Ile Ser Gln
 275 280 285
 Tyr Ile Ile Ala Gln Arg Ala Ala Gln Gly Leu Ser Thr Ser Ala Ala
 290 295 300
 Ala Ala Gly Leu Ile Ala Ser Val Val Thr Leu Ala Ile Ser Pro Leu
 305 310 315 320
 Ser Phe Leu Ser Ile Ala Asp Lys Phe Lys Arg Ala Asn Lys Ile Glu
 325 330 335
 Glu Tyr Ser Gln Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Ser Leu
 340 345 350
 Leu Ala Ala Phe His Lys Glu Thr Gly Ala Ile Asp Ala Ser Leu Thr
 355 360 365
 Arg Ile Ser Thr Val Leu Ala Ser Val Ser Ser Gly Ile Ser Ala Ala
 370 375 380
 Ala Thr Thr Ser Leu Val Gly Ala Pro Val Ser Ala Leu Val Gly Ala
 385 390 395 400
 Val Thr Gly Ile Ile Ser Gly Ile Leu Glu Ala Ser Lys Gln Ala Met
 405 410 415
 Phe Glu His Val Ala Ser Lys Met Ala Asp Val Ile Ala Glu Trp Glu
 420 425 430
 Lys Lys His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg His
 435 440 445
 Ala Ala Phe Leu Glu Asp Asn Phe Lys Ile Leu Ser Gln Tyr Asn Lys
 450 455 460
 Glu Tyr Ser Val Glu Arg Ser Val Leu Ile Thr Gln Gln His Trp Asp
 465 470 475 480

Thr Leu Ile Gly Glu Leu Ala Gly Val Thr Arg Asn Gly Asp Lys Thr
 485 490 495
 Leu Ser Gly Lys Ser Tyr Ile Asp Tyr Tyr Glu Glu Gly Lys Arg Leu
 500 505 510
 Glu Lys Lys Pro Asp Glu Phe Gln Lys Gln Val Phe Asp Pro Leu Lys
 515 520 525
 Gly Asn Ile Asp Leu Ser Asp Ser Lys Ser Ser Thr Leu Leu Lys Phe
 530 535 540
 Val Thr Pro Leu Leu Thr Pro Gly Glu Glu Ile Arg Glu Arg Arg Gln
 545 550 555 560
 Ser Gly Lys Tyr Glu Tyr Ile Thr Glu Leu Leu Val Lys Gly Val Asp
 565 570 575
 Lys Trp Thr Val Lys Gly Val Gln Asp Lys Gly Ser Val Tyr Asp Tyr
 580 585 590
 Ser Asn Leu Ile Gln His Ala Ser Val Gly Asn Asn Gln Tyr Arg Glu
 595 600 605
 Ile Arg Ile Glu Ser His Leu Gly Asp Gly Asp Asp Lys Val Phe Leu
 610 615 620
 Ser Ala Gly Ser Ala Asn Ile Tyr Ala Gly Lys Gly His Asp Val Val
 625 630 635 640
 Tyr Tyr Asp Lys Thr Asp Thr Gly Tyr Leu Thr Ile Asp Gly Thr Lys
 645 650 655
 Ala Thr Glu Ala Gly Asn Tyr Thr Val Thr Arg Val Leu Gly Gly Asp
 660 665 670
 Val Lys Val Leu Gln Glu Val Val Lys Glu Gln Glu Val Ser Val Gly
 675 680 685
 Lys Arg Thr Glu Lys Thr Gln Tyr Arg Ser Tyr Glu Phe Thr His Ile
 690 695 700
 Asn Gly Lys Asn Leu Thr Glu Thr Asp Asn Leu Tyr Ser Val Glu Glu
 705 710 715 720
 Leu Ile Gly Thr Thr Arg Ala Asp Lys Phe Phe Gly Ser Lys Phe Ala
 725 730 735
 Asp Ile Phe His Gly Ala Asp Gly Asp Asp His Ile Glu Gly Asn Asp
 740 745 750
 Gly Asn Asp Arg Leu Tyr Gly Asp Lys Gly Asn Asp Thr Leu Ser Gly
 755 760 765
 Gly Asn Gly Asp Asp Gln Leu Tyr Gly Gly Asp Gly Asn Asp Lys Leu
 770 775 780

Ile Gly Gly Ala Gly Asn Asn Tyr Leu Asn Gly Gly Asp Gly Asp Asp
 785 790 795 800
 Glu Leu Gln Val Gln Gly Asn Ser Leu Ala Lys Asn Val Leu Ser Gly
 805 810 815
 Gly Lys Gly Asn Asp Lys Leu Tyr Gly Ser Glu Gly Ala Asp Leu Leu
 820 825 830
 Asp Gly Gly Glu Gly Asn Asp Leu Leu Lys Gly Gly Tyr Gly Asn Asp
 835 840 845
 Ile Tyr Arg Tyr Leu Ser Gly Tyr Gly His His Ile Ile Asp Asp Asp
 850 855 860
 Gly Gly Lys Asp Asp Lys Leu Ser Leu Ala Asp Ile Asp Phe Arg Asp
 865 870 875 880
 Val Ala Phe Arg Arg Glu Gly Asn Asp Leu Ile Met Tyr Lys Ala Glu
 885 890 895
 Gly Asn Val Leu Ser Ile Gly His Lys Asn Gly Ile Thr Phe Lys Asn
 900 905 910
 Trp Phe Glu Lys Glu Ser Gly Asp Ile Ser Asn His Gln Ile Glu Gln
 915 920 925
 Ile Phe Asp Lys Asp Gly Arg Val Ile Thr Pro Asp Ser Leu Lys Lys
 930 935 940
 Ala Leu Glu Tyr Gln Gln Ser Asn Asn Lys Ala Ser Tyr Val Tyr Gly
 945 950 955 960
 Asn Asp Ala Leu Ala Tyr Gly Ser Gln Gly Asn Leu Asn Pro Leu Ile
 965 970 975
 Asn Glu Ile Ser Lys Ile Ile Ser Ala Ala Gly Asn Phe Asp Val Lys
 980 985 990
 Glu Glu Arg Ala Ala Ala Ser Leu Leu Gln Leu Ser Gly Asn Ala Ser
 995 1000 1005
 Asp Phe Ser Tyr Gly Arg Asn Ser Ile Thr Leu Thr Ala Ser Ala
 1010 1015 1020

<210> 6
 <211> 12
 <212> PRT
 <213> Moraxella bovis

<400> 6
 Phe Leu Ser Glu Leu Asn Lys Glu Leu Glu Ala Glu
 1 5 10

<210> 7
 <211> 12

<212> PRT

<213> *Pasteurella haemolytica*

<400> 7

Phe Leu Leu Asn Leu Asn Lys Glu Leu Gln Ala Glu
1 5 10

<210> 8

<211> 12

<212> PRT

<213> *Escherichia coli*

<400> 8

Ile Leu Ser Gln Tyr Asn Lys Glu Tyr Ser Val Glu
1 5 10

<210> 9

<211> 12

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 9

Phe Leu Ile Asn Leu Asn Lys Glu Leu Gln Ala Glu
1 5 10

<210> 10

<211> 12

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 10

Leu Leu Ser Gln Tyr Asn Lys Glu Tyr Ser Val Glu
1 5 10

<210> 11

<211> 12

<212> PRT

<213> *Actinobacillus suis*

<400> 11

Phe Leu Ile Asn Leu Asn Lys Glu Leu Gln Ala Glu
1 5 10

<210> 12

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence

<220>
 <221> MOD_RES
 <222> (3)
 <223> L, Y, A or V

<220>
 <221> MOD_RES
 <222> (7)..(8)
 <223> L, Y, A or V

<400> 12
 Phe Leu Xaa Asn Lys Glu Xaa Xaa Glu
 1 5

<210> 13
 <211> 14
 <212> PRT
 <213> Moraxella bovis

<400> 13
 Phe Asn Asp Ile Phe His Ser Gly Glu Gly Asp Asp Leu Leu
 1 5 10

<210> 14
 <211> 14
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 14
 Phe Arg Asp Ile Phe His Gly Ala Asp Gly Asp Asp Leu Leu
 1 5 10

<210> 15
 <211> 14
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 15
 Phe Asn Asp Val Phe His Gly His Asp Gly Asp Asp Leu Ile
 1 5 10

<210> 16
 <211> 14
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 16
 Phe Arg Asp Ile Phe His Gly Ala Asp Gly Asp Asp Leu Leu
 1 5 10

<210> 17
 <211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence

<220>

<221> MOD_RES

<222> (11)

<223> L or I

<400> 17

Phe Asp Phe His Gly Ala Asp Gly Asp Asp Xaa
1 5 10

<210> 18

<211> 737

<212> PRT

<213> Moraxella bovis

<400> 18

Met Gly Gly Asp Thr Ser Leu Ile Arg Leu Asn Leu Gln Thr Leu Asn
1 5 10 15Ser Asn Leu Val Met Ile Asp Tyr Ala Gln Gln Pro Ala Leu Ser Ala
20 25 30Leu Val Ile Leu Ala Lys Tyr Tyr Gly Ile Ser Ala Ser Pro Ala Asp
35 40 45Ile Met His Gln Phe Ser Asp Asn Thr Lys Gly Asp Leu Asn Glu Ile
50 55 60Glu Trp Met Leu Ala Ala Lys Lys Leu Glu Leu Lys Val Lys Ile Ile
65 70 75 80Lys Gln Pro Leu Thr Arg Leu Ser Met Ile Thr Leu Pro Ala Leu Val
85 90 95Trp Cys Asp Asn Lys Pro Asp Leu Asp Gln Asn Leu Asn Ser His Phe
100 105 110Ile Leu Thr Lys Ile Asp Gly Val Gly Ser Ala Ala Lys Tyr Leu Ile
115 120 125Tyr Asp Leu Ile Glu Asn Arg Pro Ile Ile Leu Asp Ala Ser Glu Phe
130 135 140Ser Glu Arg Tyr Ser Gly Lys Leu Met Leu Val Thr Ser Arg Ala Ser
145 150 155 160Ile Leu Gly Ser Leu Ala Lys Phe Asp Phe Thr Trp Phe Ile Pro Ala
165 170 175Val Ile Lys Tyr Arg Tyr Ile Phe Phe Glu Val Ile Val Ile Ser Val
180 185 190

Val Leu Gln Ile Phe Ala Leu Ile Thr Pro Leu Phe Phe Gln Val Val
 195 200 205
 Met Asp Lys Val Leu Val His Arg Gly Phe Ser Thr Leu Asp Val Val
 210 215 220
 Ala Ile Ala Leu Leu Val Val Ser Leu Phe Glu Val Ile Leu Ser Gly
 225 230 235 240
 Leu Arg Thr Tyr Ile Phe Ala His Thr Thr Ser Arg Ile Asp Val Glu
 245 250 255
 Leu Gly Ala Arg Leu Phe Arg His Leu Leu Ala Leu Pro Leu Ala Tyr
 260 265 270
 Phe Glu Ser Arg Arg Val Gly Asp Thr Val Ala Arg Ile Arg Glu Leu
 275 280 285
 Glu His Ile Arg Asn Phe Leu Thr Gly Gln Ala Leu Thr Ser Val Leu
 290 295 300
 Asp Leu Val Phe Ser Phe Ile Phe Leu Phe Val Met Trp Tyr Tyr Ser
 305 310 315 320
 Pro Thr Leu Thr Leu Val Val Leu Ala Ser Leu Pro Ile Tyr Ala Phe
 325 330 335
 Trp Ser Ala Phe Ile Ser Pro Ile Leu Arg Thr Arg Leu Asn Asp Gln
 340 345 350
 Phe Ala Arg Asn Ala Asp Asn Gln Ser Phe Leu Val Glu Ser Ile Thr
 355 360 365
 Ala Val Gly Thr Val Lys Ala Met Ala Val Glu Pro Gln Met Thr Arg
 370 375 380
 Arg Trp Asp Asn Gln Leu Ala Ala Tyr Val Val Ser Ser Phe Arg Val
 385 390 395 400
 Ala Lys Leu Ala Met Val Gly Gln Gln Gly Val Gln Leu Ile Gln Lys
 405 410 415
 Met Val Ile Val Ala Thr Leu Trp Ile Gly Ala Lys Leu Val Ile Glu
 420 425 430
 Gly Lys Leu Ser Val Gly Gln Leu Ile Ala Phe Asn Met Leu Ala Gly
 435 440 445
 Gln Val Ala Ala Pro Val Ile Arg Leu Ala Gln Leu Trp Gln Asp Phe
 450 455 460
 Gln Gln Val Gly Ile Ser Val Ala Arg Leu Gly Asp Ile Leu Asn Thr
 465 470 475 480
 Pro Thr Glu His Ser Thr Ser Arg Leu Thr Leu Pro Asp Ile Lys Gly
 485 490 495

Asp Ile Thr Phe Glu Asn Val Asp Phe Arg Tyr Lys Ile Asp Gly His
 500 505 510
 Leu Ile Leu Gln Asn Leu Asn Leu Gln Ile Asn Ala Gly Glu Ile Leu
 515 520 525
 Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser Thr Leu Thr Lys Leu
 530 535 540
 Val Gln Arg Leu Tyr Val Pro Glu Asn Gly Arg Ile Leu Val Asp Gly
 545 550 555 560
 Asn Asp Leu Ala Leu Ala Asp Pro Ala Trp Leu Arg Arg Gln Val Gly
 565 570 575
 Val Val Leu Gln Glu Asn Val Leu Leu Asn Arg Ser Ile Arg Asp Asn
 580 585 590
 Ile Ala Leu Thr Asp Thr Gly Met Ser Leu Glu Phe Ile Ile Gln Ala
 595 600 605
 Ala Lys Met Ser Gly Ala His Asp Phe Ile Met Glu Leu Pro Glu Gly
 610 615 620
 Tyr Asp Thr Ile Val Gly Glu Gln Gly Ala Gly Leu Ser Gly Gly Gln
 625 630 635 640
 Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Ile Thr Asn Pro Arg Ile
 645 650 655
 Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp Tyr Glu Ser Glu Arg
 660 665 670
 Ala Ile Met Gln Asn Met Gln Ala Ile Cys Gln Gly Arg Thr Val Leu
 675 680 685
 Ile Ile Ala His Arg Leu Ser Thr Val Lys Met Ala His Arg Ile Ile
 690 695 700
 Ala Met Asp Lys Gly Lys Ile Val Glu Gln Gly Thr His Gln Glu Leu
 705 710 715 720
 Leu Gln Lys Glu Asp Gly Tyr Tyr Arg Tyr Leu Tyr Asp Leu Gln Asn
 725 730 735

Gly

<210> 19

<211> 708

<212> PRT

<213> *Pasteurella haemolytica*

<400> 19

Met Glu Ala Asn His Gln Arg Asn Asp Leu Gly Leu Val Ala Leu Thr
 1 5 10 15

Met	Leu	Ala	Gln	Tyr	His	Asn	Ile	Ser	Leu	Asn	Pro	Glu	Glu	Ile	Lys	20	25	30
His	Lys	Phe	Asp	Leu	Asp	Gly	Lys	Gly	Leu	Ser	Leu	Thr	Ala	Trp	Leu	35	40	45
Leu	Ala	Ala	Lys	Ser	Leu	Ala	Leu	Lys	Ala	Lys	His	Ile	Lys	Lys	Glu	50	55	60
Ile	Ser	Arg	Leu	His	Leu	Val	Asn	Leu	Pro	Ala	Leu	Val	Trp	Gln	Asp	65	70	75
Asn	Gly	Lys	His	Phe	Leu	Leu	Val	Lys	Val	Asp	Thr	Asp	Asn	Asn	Arg	85	90	95
Tyr	Leu	Thr	Tyr	Asn	Leu	Glu	Gln	Asp	Ala	Pro	Gln	Ile	Leu	Ser	Thr	100	105	110
Asp	Glu	Phe	Glu	Ala	Cys	Tyr	Gln	Gly	Gln	Leu	Ile	Leu	Val	Thr	Ser	115	120	125
Arg	Ala	Ser	Val	Val	Gly	Gln	Leu	Ala	Lys	Phe	Asp	Phe	Thr	Trp	Phe	130	135	140
Ile	Pro	Ala	Val	Ile	Lys	Tyr	Arg	Lys	Ile	Phe	Leu	Glu	Thr	Leu	Ile	145	150	155
Val	Ser	Ile	Phe	Leu	Gln	Ile	Phe	Ala	Leu	Ile	Thr	Pro	Leu	Phe	Phe	165	170	175
Gln	Val	Val	Met	Asp	Lys	Val	Leu	Val	His	Arg	Gly	Phe	Ser	Thr	Leu	180	185	190
Asn	Ile	Ile	Thr	Val	Ala	Leu	Ala	Ile	Val	Ile	Ile	Phe	Glu	Ile	Val	195	200	205
Leu	Ser	Gly	Leu	Arg	Thr	Tyr	Val	Phe	Ser	His	Ser	Thr	Ser	Arg	Ile	210	215	220
Asp	Val	Glu	Leu	Gly	Ala	Lys	Leu	Phe	Arg	His	Leu	Leu	Ser	Leu	Pro	225	230	235
Ile	Ser	Tyr	Phe	Glu	Asn	Arg	Arg	Val	Gly	Asp	Thr	Val	Ala	Arg	Val	245	250	255
Arg	Glu	Leu	Asp	Gln	Ile	Arg	Asn	Phe	Leu	Thr	Gly	Gln	Ala	Leu	Thr	260	265	270
Ser	Val	Leu	Asp	Leu	Leu	Phe	Ser	Phe	Ile	Phe	Phe	Ala	Val	Met	Trp	275	280	285
Tyr	Tyr	Ser	Pro	Lys	Leu	Thr	Leu	Val	Ile	Leu	Gly	Ser	Leu	Pro	Cys	290	295	300
Tyr	Ile	Leu	Trp	Ser	Ile	Phe	Ile	Ser	Pro	Ile	Leu	Arg	Arg	Arg	Leu	305	310	315
																		320

Asp Glu Lys Phe Ala Arg Ser Ala Asp Asn Gln Ala Phe Leu Val Glu
 325 330 335
 Ser Val Thr Ala Ile Asn Met Ile Lys Ala Met Ala Val Ala Pro Gln
 340 345 350
 Met Thr Asp Thr Trp Asp Lys Gln Leu Ala Ser Tyr Val Ser Ser Ser
 355 360 365
 Phe Arg Val Thr Val Leu Ala Thr Ile Gly Gln Gln Gly Val Gln Leu
 370 375 380
 Ile Gln Lys Thr Val Met Val Ile Asn Leu Trp Leu Gly Ala His Leu
 385 390 395 400
 Val Ile Ser Gly Asp Leu Ser Ile Gly Gln Leu Ile Ala Phe Asn Met
 405 410 415
 Leu Ser Gly Gln Val Ile Ala Pro Val Ile Arg Leu Ala Gln Leu Trp
 420 425 430
 Gln Asp Phe Gln Gln Val Gly Ile Ser Val Thr Arg Leu Gly Asp Val
 435 440 445
 Leu Asn Ser Pro Thr Glu Gln Tyr Gln Gly Lys Leu Ser Leu Pro Glu
 450 455 460
 Ile Lys Gly Asp Ile Ser Phe Lys Asn Ile Arg Phe Arg Tyr Lys Pro
 465 470 475 480
 Asp Ala Pro Thr Ile Leu Asn Asn Val Asn Leu Glu Ile Arg Gln Gly
 485 490 495
 Glu Val Ile Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser Thr Leu
 500 505 510
 Thr Lys Leu Leu Gln Arg Phe Tyr Ile Pro Glu Asn Gly Gln Val Leu
 515 520 525
 Ile Asp Gly His Asp Leu Ala Leu Ala Asp Pro Asn Trp Leu Arg Arg
 530 535 540
 Gln Ile Gly Val Val Leu Gln Asp Asn Val Leu Leu Asn Arg Ser Ile
 545 550 555 560
 Arg Glu Asn Ile Ala Leu Ser Asp Pro Gly Met Pro Met Glu Arg Val
 565 570 575
 Ile Tyr Ala Ala Lys Leu Ala Gly Ala His Asp Phe Ile Ser Glu Leu
 580 585 590
 Arg Glu Gly Tyr Asn Thr Ile Val Gly Glu Gln Gly Ala Gly Leu Ser
 595 600 605
 Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Asn Asn
 610 615 620

Pro Lys Ile Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp Tyr Glu
625 630 635 640

Ser Glu His Ile Ile Met Gln Asn Met Gln Lys Ile Cys Gln Gly Arg
645 650 655

Thr Val Ile Leu Ile Ala His Arg Leu Ser Thr Val Lys Asn Ala Asp
660 665 670

Arg Ile Ile Val Met Glu Lys Gly Glu Ile Val Glu Gln Gly Lys His
675 680 685

His Glu Leu Leu Gln Asn Ser Asn Gly Leu Tyr Ser Tyr Leu His Gln
690 695 700

Leu Gln Leu Asn
705

<210> 20

<211> 707

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 20

Met Asp Phe Tyr Arg Glu Glu Asp Tyr Gly Leu Tyr Ala Leu Thr Ile
1 5 10 15

Leu Ala Gln Tyr His Asn Ile Ala Val Asn Pro Glu Glu Leu Lys His
20 25 30

Lys Phe Asp Leu Glu Gly Lys Gly Leu Asp Leu Thr Ala Trp Leu Leu
35 40 45

Ala Ala Lys Ser Leu Glu Leu Lys Ala Lys Gln Val Lys Lys Ala Ile
50 55 60

Asp Arg Leu Ala Phe Ile Ala Leu Pro Ala Leu Val Trp Arg Glu Asp
65 70 75 80

Gly Lys His Phe Ile Leu Thr Lys Ile Asp Asn Glu Ala Lys Lys Tyr
85 90 95

Leu Ile Phe Asp Leu Glu Thr His Asn Pro Arg Ile Leu Glu Gln Ala
100 105 110

Glu Phe Glu Ser Leu Tyr Gln Gly Lys Leu Ile Leu Val Ala Ser Arg
115 120 125

Ala Ser Ile Val Gly Lys Leu Ala Lys Phe Asp Phe Thr Trp Phe Ile
130 135 140

Pro Ala Val Ile Lys Tyr Arg Lys Ile Phe Ile Glu Thr Leu Ile Val
145 150 155 160

Ser Ile Phe Leu Gln Ile Phe Ala Leu Ile Thr Pro Leu Phe Phe Gln
165 170 175

Val	Val	Met	Asp	Lys	Val	Leu	Val	His	Arg	Gly	Phe	Ser	Thr	Leu	Asn	180	185	190
Val	Ile	Thr	Val	Ala	Leu	Ala	Ile	Val	Val	Leu	Phe	Glu	Ile	Val	Leu	195	200	205
Asn	Gly	Leu	Arg	Thr	Tyr	Ile	Phe	Ala	His	Ser	Thr	Ser	Arg	Ile	Asp	210	215	220
Val	Glu	Leu	Gly	Ala	Arg	Leu	Phe	Arg	His	Leu	Leu	Ala	Leu	Pro	Ile	225	230	235
Ser	Tyr	Phe	Glu	Asn	Arg	Arg	Val	Gly	Asp	Thr	Val	Ala	Arg	Val	Arg	245	250	255
Glu	Leu	Asp	Gln	Ile	Arg	Asn	Phe	Leu	Thr	Gly	Gln	Ala	Leu	Thr	Ser	260	265	270
Val	Leu	Asp	Leu	Met	Phe	Ser	Phe	Ile	Phe	Phe	Ala	Val	Met	Trp	Tyr	275	280	285
Tyr	Ser	Pro	Lys	Leu	Thr	Leu	Val	Ile	Leu	Gly	Ser	Leu	Pro	Phe	Tyr	290	295	300
Met	Gly	Trp	Ser	Ile	Phe	Ile	Ser	Pro	Ile	Leu	Arg	Arg	Arg	Leu	Asp	305	310	315
Glu	Lys	Phe	Ala	Arg	Gly	Ala	Asp	Asn	Gln	Ser	Phe	Leu	Val	Glu	Ser	325	330	335
Val	Thr	Ala	Ile	Asn	Thr	Ile	Lys	Ala	Leu	Ala	Val	Thr	Pro	Gln	Met	340	345	350
Thr	Asn	Thr	Trp	Asp	Lys	Gln	Leu	Ala	Ser	Tyr	Val	Ser	Ala	Gly	Phe	355	360	365
Arg	Val	Thr	Thr	Leu	Ala	Thr	Ile	Gly	Gln	Gln	Gly	Val	Gln	Phe	Ile	370	375	380
Gln	Lys	Val	Val	Met	Val	Ile	Thr	Leu	Trp	Leu	Gly	Ala	His	Leu	Val	385	390	395
Ile	Ser	Gly	Asp	Leu	Ser	Ile	Gly	Gln	Leu	Ile	Ala	Phe	Asn	Met	Leu	405	410	415
Ser	Gly	Gln	Val	Ile	Ala	Pro	Val	Ile	Arg	Leu	Ala	Gln	Leu	Trp	Gln	420	425	430
Asp	Phe	Gln	Gln	Val	Gly	Ile	Ser	Val	Thr	Arg	Leu	Gly	Asp	Val	Leu	435	440	445
Asn	Ser	Pro	Thr	Glu	Ser	Tyr	Gln	Gly	Lys	Leu	Ala	Leu	Pro	Glu	Ile	450	455	460
Lys	Gly	Asp	Ile	Thr	Phe	Arg	Asn	Ile	Arg	Phe	Arg	Tyr	Lys	Pro	Asp	465	470	475

Ala Pro Val Ile Leu Asn Asp Val Asn Leu Ser Ile Gln Gln Gly Glu
 485 490 495
 Val Ile Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser Thr Leu Thr
 500 505 510
 Lys Leu Ile Gln Arg Phe Tyr Ile Pro Glu Asn Gly Gln Val Leu Ile
 515 520 525
 Asp Gly His Asp Leu Ala Leu Ala Asp Pro Asn Trp Leu Arg Arg Gln
 530 535 540
 Val Gly Val Val Leu Gln Asp Asn Val Leu Leu Asn Arg Ser Ile Arg
 545 550 555 560
 Asp Asn Ile Ala Leu Ala Asp Pro Gly Met Pro Met Glu Lys Ile Val
 565 570 575
 His Ala Ala Lys Leu Ala Gly Ala His Glu Phe Ile Ser Glu Leu Arg
 580 585 590
 Glu Gly Tyr Asn Thr Ile Val Gly Glu Gln Gly Ala Gly Leu Ser Gly
 595 600 605
 Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Asn Asn Pro
 610 615 620
 Lys Ile Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp Tyr Glu Ser
 625 630 635 640
 Glu His Ile Ile Met Arg Asn Met His Gln Ile Cys Lys Gly Arg Thr
 645 650 655
 Val Ile Ile Ile Ala His Arg Leu Ser Thr Val Lys Asn Ala Asp Arg
 660 665 670
 Ile Ile Val Met Glu Lys Gly Gln Ile Val Glu Gln Gly Lys His Lys
 675 680 685
 Glu Leu Leu Ala Asp Pro Asn Gly Leu Tyr His Tyr Leu His Gln Leu
 690 695 700
 Gln Ser Glu
 705

<210> 21
 <211> 707
 <212> PRT
 <213> Escherichia coli

<400> 21
 Met Asp Ser Cys His Lys Ile Asp Tyr Gly Leu Tyr Ala Leu Glu Ile
 1 5 10 15
 Leu Ala Gln Tyr His Asn Val Ser Val Asn Pro Glu Glu Ile Lys His
 20 25 30

Arg Phe Asp Thr Asp Gly Thr Gly Leu Gly Leu Thr Ser Trp Leu Leu
 35 40 45
 Ala Ala Lys Ser Leu Glu Leu Lys Val Lys Gln Val Lys Lys Thr Ile
 50 55 60
 Asp Arg Leu Asn Phe Ile Ser Leu Pro Ala Leu Val Trp Arg Glu Asp
 65 70 75 80
 Gly Arg His Phe Ile Leu Thr Lys Val Ser Lys Glu Ala Asn Arg Tyr
 85 90 95
 Leu Ile Phe Asp Leu Glu Gln Arg Asn Pro Arg Val Leu Glu Gln Ser
 100 105 110
 Glu Phe Glu Ala Leu Tyr Gln Gly His Ile Ile Leu Ile Ala Ser Arg
 115 120 125
 Ser Ser Val Ala Gly Lys Leu Ala Lys Phe Asp Phe Thr Trp Phe Ile
 130 135 140
 Pro Ala Ile Ile Lys Tyr Arg Arg Ile Phe Ile Glu Thr Leu Val Val
 145 150 155 160
 Ser Val Phe Leu Gln Leu Phe Ala Leu Ile Thr Pro Leu Phe Phe Gln
 165 170 175
 Val Val Met Asp Lys Val Leu Val His Arg Gly Phe Ser Thr Leu Asn
 180 185 190
 Val Ile Thr Val Ala Leu Ser Val Val Val Val Phe Glu Ile Ile Leu
 195 200 205
 Ser Gly Leu Arg Thr Tyr Ile Phe Ala His Ser Thr Ser Arg Ile Asp
 210 215 220
 Val Glu Leu Gly Ala Lys Leu Phe Arg His Leu Leu Ala Leu Pro Ile
 225 230 235 240
 Ser Tyr Phe Glu Ser Arg Arg Val Gly Asp Thr Val Ala Arg Val Arg
 245 250 255
 Glu Leu Asp Gln Ile Arg Asn Phe Leu Thr Gly Gln Ala Leu Thr Ser
 260 265 270
 Val Leu Asp Leu Leu Phe Ser Phe Ile Phe Phe Ala Val Met Trp Tyr
 275 280 285
 Tyr Ser Pro Lys Leu Thr Leu Val Ile Leu Phe Ser Leu Pro Cys Tyr
 290 295 300
 Ala Ala Trp Ser Val Phe Ile Ser Pro Ile Leu Arg Arg Arg Leu Asp
 305 310 315 320
 Asp Lys Phe Ser Arg Asn Ala Asp Asn Gln Ser Phe Leu Val Glu Ser
 325 330 335

Val	Thr	Ala	Ile	Asn	Thr	Ile	Lys	Ala	Met	Ala	Val	Ser	Pro	Gln	Met	340	345	350
Thr	Asn	Ile	Trp	Asp	Lys	Gln	Leu	Ala	Gly	Tyr	Val	Ala	Ala	Gly	Phe	355	360	365
Lys	Val	Thr	Val	Leu	Ala	Thr	Ile	Gly	Gln	Gln	Gly	Ile	Gln	Leu	Ile	370	375	380
Gln	Lys	Thr	Val	Met	Ile	Ile	Asn	Leu	Trp	Leu	Gly	Ala	His	Leu	Val	385	390	395
Ile	Ser	Gly	Asp	Leu	Ser	Ile	Gly	Gln	Leu	Ile	Ala	Phe	Asn	Met	Leu	405	410	415
Ala	Gly	Gln	Ile	Val	Ala	Pro	Val	Ile	Arg	Leu	Ala	Gln	Ile	Trp	Gln	420	425	430
Asp	Phe	Gln	Gln	Val	Gly	Ile	Ser	Val	Thr	Arg	Leu	Gly	Asp	Val	Leu	435	440	445
Asn	Ser	Pro	Thr	Glu	Ser	Tyr	His	Gly	Lys	Leu	Ala	Leu	Pro	Glu	Ile	450	455	460
Asn	Gly	Asp	Ile	Thr	Phe	Arg	Asn	Ile	Arg	Phe	Arg	Tyr	Lys	Pro	Asp	465	470	475
Ser	Pro	Val	Ile	Leu	Asp	Asn	Ile	Asn	Leu	Ser	Ile	Lys	Gln	Gly	Glu	485	490	495
Val	Ile	Gly	Ile	Val	Gly	Arg	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Thr	500	505	510
Lys	Leu	Ile	Gln	Arg	Phe	Tyr	Ile	Pro	Glu	Asn	Gly	Gln	Val	Leu	Ile	515	520	525
Asp	Gly	His	Asp	Leu	Ala	Leu	Ala	Asp	Pro	Asn	Trp	Leu	Arg	Arg	Gln	530	535	540
Val	Gly	Val	Val	Leu	Gln	Asp	Asn	Val	Leu	Leu	Asn	Arg	Ser	Ile	Ile	545	550	555
Asp	Asn	Ile	Ser	Leu	Ala	Asn	Pro	Gly	Met	Ser	Val	Glu	Lys	Val	Ile	565	570	575
Tyr	Ala	Ala	Lys	Leu	Ala	Gly	Ala	His	Asp	Phe	Ile	Ser	Glu	Leu	Arg	580	585	590
Glu	Gly	Tyr	Asn	Thr	Ile	Val	Gly	Glu	Gln	Gly	Ala	Gly	Leu	Ser	Gly	595	600	605
Gly	Gln	Arg	Gln	Arg	Ile	Ala	Ile	Ala	Arg	Ala	Leu	Val	Asn	Asn	Pro	610	615	620
Lys	Ile	Leu	Ile	Phe	Asp	Glu	Ala	Thr	Ser	Ala	Leu	Asp	Tyr	Glu	Ser	625	630	635

Glu His Ile Ile Met Arg Asn Met His Lys Ile Cys Lys Gly Arg Thr
 645 650 655

Val Ile Ile Ile Ala His Arg Leu Ser Thr Val Lys Asn Ala Asp Arg
 660 665 670

Ile Ile Val Met Glu Lys Gly Lys Ile Val Glu Gln Gly Lys His Lys
 675 680 685

Glu Leu Leu Ser Glu Pro Glu Ser Leu Tyr Ser Tyr Leu Tyr Gln Leu
 690 695 700

Gln Ser Asp
 705

<210> 22
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 22
 aatgacgata tctttgttgg tcaaggtaaa

30

<210> 23
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> modified_base
 <222> (18)
 <223> a, t, c, g, other or unknown

<400> 23
 aayaaagart trgargcnga r

21

<210> 24
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> modified_base
 <222> (6)
 <223> a, t, c, g, other or unknown

<400> 24
ccytcnccrc trtgraadat rtcrtttraat tt

32

<210> 25
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> modified_base
<222> (15)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (18)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (24)
<223> a, t, c, g, other or unknown

<400> 25
athgaytgga thgcncntt yggngay

27

<210> 26
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
actttatcca tcacracttg raaraa

26

<210> 27
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
gatcatatgt ccaatataaa tgtaattaa tctaa

35

<210> 28
<211> 30

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 28
 atcactagtt ccataatcta taaccaatga

30

<210> 29
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: consensus
 sequence

<220>
 <221> MOD_RES
 <222> (1)..(2)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (5)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (7)
 <223> N or D

<220>
 <221> MOD_RES
 <222> (9)
 <223> Any amino acid

<400> 29
 Xaa Xaa Gly Gly Xaa Gly Xaa Asp Xaa
 1 5

<210> 30
 <211> 2215
 <212> DNA
 <213> Moraxella bovis

<220>
 <221> CDS
 <222> (1)..(2211)

<400> 30
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 Met Gly Gly Asp Thr Ser Leu Ile Arg Leu Asn Leu Gln Thr Leu Asn
 1 5 10 15

agt aat tta gtt atg ata gat tat gct caa caa cct gct cta tct gct	96
Ser Asn Leu Val Met Ile Asp Tyr Ala Gln Gln Pro Ala Leu Ser Ala	
20 25 30	
ctg gtt atc ctt gcc aaa tac tat ggt att tct gca agt cca gca gac	144
Leu Val Ile Leu Ala Lys Tyr Tyr Gly Ile Ser Ala Ser Pro Ala Asp	
35 40 45	
att atg cat cag ttt tct gat aat aca aaa gga gac ctg aat gaa att	192
Ile Met His Gln Phe Ser Asp Asn Thr Lys Gly Asp Leu Asn Glu Ile	
50 55 60	
gaa tgg atg ttg gca gca aag aaa tta gaa tta aag gta aag att ata	240
Glu Trp Met Leu Ala Ala Lys Lys Leu Glu Leu Lys Val Lys Ile Ile	
65 70 75 80	
aaa cag cct tta act cga ttg tca atg ata aca ctt cct gct ttg gtg	288
Lys Gln Pro Leu Thr Arg Leu Ser Met Ile Thr Leu Pro Ala Leu Val	
85 90 95	
tgg tgt gat aat aag ccc gat tta gat caa aat tta aac tct cat ttt	336
Trp Cys Asp Asn Lys Pro Asp Leu Asp Gln Asn Leu Asn Ser His Phe	
100 105 110	
ata cta act aaa att gat ggg gtg gga tct gct gca aaa tat ctc atc	384
Ile Leu Thr Lys Ile Asp Gly Val Gly Ser Ala Ala Lys Tyr Leu Ile	
115 120 125	
tac gat ttg att gag aat cgt ccc ata ata tta gat gca agt gag ttt	432
Tyr Asp Leu Ile Glu Asn Arg Pro Ile Ile Leu Asp Ala Ser Glu Phe	
130 135 140	
tct gaa aga tat tct ggt aag tta atg cta gta act tcc cgt gcg tca	480
Ser Glu Arg Tyr Ser Gly Lys Leu Met Leu Val Thr Ser Arg Ala Ser	
145 150 155 160	
ata ttg ggt tca ttg gct aaa ttt gat ttt act tgg ttt att cct gcg	528
Ile Leu Gly Ser Leu Ala Lys Phe Asp Phe Thr Trp Phe Ile Pro Ala	
165 170 175	
gta atc aaa tat cgt tat att ttt ttt gaa gtc atc gtt att tca gtg	576
Val Ile Lys Tyr Arg Tyr Ile Phe Phe Glu Val Ile Val Ile Ser Val	
180 185 190	
gtg cta cag att ttt gct ctg att acg cca ttg ttt ttt cag gtt gtg	624
Val Leu Gln Ile Phe Ala Leu Ile Thr Pro Leu Phe Phe Gln Val Val	
195 200 205	
atg gat aag gta ttg gtg cat cgt ggt ttt tct act ctg gat gtg gta	672
Met Asp Lys Val Leu Val His Arg Gly Phe Ser Thr Leu Asp Val Val	
210 215 220	
gcg att gcc ttg ttg gta gta agt tta ttt gaa gtc att tta agt ggt	720
Ala Ile Ala Leu Leu Val Val Ser Leu Phe Glu Val Ile Leu Ser Gly	
225 230 235 240	

cta cgc act tat att ttt gct cat aca acc tct cga att gat gta gag	768
Leu Arg Thr Tyr Ile Phe Ala His Thr Thr Ser Arg Ile Asp Val Glu	
245 250 255	
cta gga gca cga tta ttt cgt cat cta tta gct cta ccg ctt gct tat	816
Leu Gly Ala Arg Leu Phe Arg His Leu Leu Ala Leu Pro Leu Ala Tyr	
260 265 270	
ttt gag agt aga aga gta ggc gat aca gtt gca cgt ata cgt gaa ttg	864
Phe Glu Ser Arg Arg Val Gly Asp Thr Val Ala Arg Ile Arg Glu Leu	
275 280 285	
gaa cat atc cgc aat ttc tta act ggt caa gct ctc act tca gtt tta	912
Glu His Ile Arg Asn Phe Leu Thr Gly Gln Ala Leu Thr Ser Val Leu	
290 295 300	
gat ttg gtg ttt tct ttt ata ttc ttg ttt gta atg tgg tat tac agc	960
Asp Leu Val Phe Ser Phe Ile Phe Leu Phe Val Met Trp Tyr Tyr Ser	
305 310 315 320	
cct act tta aca ctg gta gtt ttg gca tca tta cca ata tat gcg ttt	1008
Pro Thr Leu Thr Leu Val Val Leu Ala Ser Leu Pro Ile Tyr Ala Phe	
325 330 335	
tgg tct gcc ttt att agc cca att tta cgc act cga cta aat gat caa	1056
Trp Ser Ala Phe Ile Ser Pro Ile Leu Arg Thr Arg Leu Asn Asp Gln	
340 345 350	
ttt gca cgc aat gca gat aat caa tct ttt tta gtg gaa agt att act	1104
Phe Ala Arg Asn Ala Asp Asn Gln Ser Phe Leu Val Glu Ser Ile Thr	
355 360 365	
gcg gtt ggt acg gta aaa gca atg gca gtt gaa cct caa atg acc cgt	1152
Ala Val Gly Thr Val Lys Ala Met Ala Val Glu Pro Gln Met Thr Arg	
370 375 380	
cgc tgg gat aat caa tta gca gct tat gtg gtt tct agt ttt cgg gta	1200
Arg Trp Asp Asn Gln Leu Ala Ala Tyr Val Val Ser Ser Phe Arg Val	
385 390 395 400	
gct aag ttg gca atg gtt ggg cag caa gga gta caa ctc att caa aag	1248
Ala Lys Leu Ala Met Val Gly Gln Gln Gly Val Gln Leu Ile Gln Lys	
405 410 415	
atg gtt att gtg gca act cta tgg att ggt gca aaa ttg gta att gaa	1296
Met Val Ile Val Ala Thr Leu Trp Ile Gly Ala Lys Leu Val Ile Glu	
420 425 430	
ggc aag cta tcg gta ggt caa tta ata gca ttt aat atg ctg gca ggt	1344
Gly Lys Leu Ser Val Gly Gln Leu Ile Ala Phe Asn Met Leu Ala Gly	
435 440 445	
cag gtg gcc gct cct gtt atc cgc ctg gca cag cta tgg caa gat ttt	1392
Gln Val Ala Ala Pro Val Ile Arg Leu Ala Gln Leu Trp Gln Asp Phe	
450 455 460	

cag Gln 465	caa Gln	gta Val	ggg Gly	att Ile	tca Ser 470	gtg Val	gag Ala	aga Arg	ttg Leu 475	ggg Gly	gat Asp	att Ile	tta Leu	aat Asn	act Thr 480	1440
cca Pro	act Thr	gag Glu	cat His	tct Ser 485	aca Thr	tct Ser	cgc Arg	tta Leu	act Thr 490	tta Leu	cct Pro	gat Asp	att Ile	aag Lys 495	ggg Gly	1488
gat Asp	att Ile	aca Thr 500	ttt Phe	gaa Glu	aat Asn	gtt Val	gat Asp	ttt Phe 505	cgc Arg	tac Tyr	aaa Lys	ata Ile	gat Asp 510	ggg Gly	cat His	1536
tta Leu	ata Ile	tta Leu 515	cag Gln	aat Asn	tta Leu	aat Asn	tta Leu	cag Gln 520	att Ile	aac Asn	gct Ala	gga Gly 525	gag Glu	ata Ile	cta Leu	1584
ggg Gly 530	atc Ile	gta Val	gga Gly	cgc Arg	tct Ser	ggg Gly 535	tca Ser	ggg Gly	aaa Lys	tca Ser	aca Thr 540	ttg Leu	aca Thr	aaa Lys	tta Leu	1632
gta Val 545	cag Gln	cgt Arg	tta Leu	tat Tyr	gta Val 550	cca Pro	gaa Glu	aat Asn	ggg Gly	cga Arg 555	ata Ile	tta Leu	gtt Val	gat Asp	gga Gly 560	1680
aac Asn	gat Asp	ttg Leu	gca Ala	tta Leu 565	gct Ala	gat Asp	ccc Pro	gct Ala 570	tgg Trp	ctg Leu	cgt Arg	cgc Arg	caa Gln	gtg Val 575	ggg Gly	1728
gtt Val	gtt Val	ttg Leu	cag Gln 580	gaa Glu	aat Asn	gtg Val	tta Leu	ctc Leu 585	aat Asn	cgt Arg	agt Ser	att Ile	cga Arg 590	gat Asp	aat Asn	1776
att Ile	gcc Ala	cta Leu 595	act Thr	gat Asp	acg Thr	ggc Gly	atg Met 600	tca Ser	tta Leu	gag Glu	ttt Phe	att Ile 605	atc Gln	cag Ala	gct Ala	1824
gcc Ala 610	aag Lys	atg Met	tct Ser	ggg Gly	gca Ala	cat His	gac Asp 615	ttt Phe	att Ile	atg Met 620	gaa Glu	ttg Leu	cct Pro	gag Glu	ggg Gly	1872
tat Tyr 625	gat Asp	acg Thr	att Ile	gtt Val	gga Gly	gag Glu	caa Gln	ggg Gly	gca Ala	ggc Gly 635	ttg Leu	tca Ser	ggg Gly	gga Gly	caa Gln 640	1920
cgc Arg	cag Gln	cgt Arg	atc Ile	gct Ala 645	att Ile	gag Ala	cgt Arg	gct Ala	tta Leu 650	att Ile	acc Thr	aat Asn	ccg Pro	cgt Arg 655	att Ile	1968
ttg Leu	att Ile	ttt Phe	gat Asp 660	gaa Glu	gct Ala	act Thr	agt Ser	gca Ala 665	tta Leu	gac Asp	tat Tyr	gag Glu	tcg Ser 670	gaa Glu	agg Arg	2016
gct Ala	att Ile	atg Met 675	caa Gln	aat Asn	atg Met	cag Gln	gca Ala 680	att Ile	tgc Cys	caa Gln	ggg Gly	aga Arg 685	aca Thr	gtg Val	ttg Leu	2064

att att gca cat cgc tta tct acc gta aaa atg gca cat cgc att att	2112
Ile Ile Ala His Arg Leu Ser Thr Val Lys Met Ala His Arg Ile Ile	
690 695 700	

gca atg gac aag ggg aaa att gta gag caa ggc aca cat caa gaa ttg	2160
Ala Met Asp Lys Gly Lys Ile Val Glu Gln Gly Thr His Gln Glu Leu	
705 710 715 720	

ttg caa aaa gaa gat ggt tac tat cgt tat tta tat gat ttg cag aat	2208
Leu Gln Lys Glu Asp Gly Tyr Tyr Arg Tyr Leu Tyr Asp Leu Gln Asn	
725 730 735	

gga taaa	2215
Gly	

<210> 31

<211> 507

<212> DNA

<213> Moraxella bovis

<220>

<221> CDS

<222> (1) .. (504)

<400> 31

atg acg aaa aag ttt gca gag cta ggt tta att gca tgg ctt tgg tct	48
Met Thr Lys Lys Phe Ala Glu Leu Gly Leu Ile Ala Trp Leu Trp Ser	
1 5 10 15	

aac tct gat atg cat aaa cat tgg acg ttg tct ttg ttt gcg acc aat	96
Asn Ser Asp Met His Lys His Trp Thr Leu Ser Leu Phe Ala Thr Asn	
20 25 30	

gtt att ccg gca att gag aca ggt caa tat gtt ata ttg aaa aga gaa	144
Val Ile Pro Ala Ile Glu Thr Gly Gln Tyr Val Ile Leu Lys Arg Glu	
35 40 45	

gat atg cct gta gca tat tgt agt tgg gct aaa ctt agt tta gaa aac	192
Asp Met Pro Val Ala Tyr Cys Ser Trp Ala Lys Leu Ser Leu Glu Asn	
50 55 60	

gag gtt aaa tat att aac gat gtt act tct ctt aag tta gat gac tgg	240
Glu Val Lys Tyr Ile Asn Asp Val Thr Ser Leu Lys Leu Asp Asp Trp	
65 70 75 80	

cag tca ggt gac cga aac tgg ttt att gac tgg att gct cca ttt ggc	288
Gln Ser Gly Asp Arg Asn Trp Phe Ile Asp Trp Ile Ala Pro Phe Gly	
85 90 95	

gat agt ctt aca ctc aca aaa cac atg aga acg tta ttt tca gat gaa	336
Asp Ser Leu Thr Leu Thr Lys His Met Arg Thr Leu Phe Ser Asp Glu	
100 105 110	

ttg ttt aga gcg att cgt gta gat gga aat tca tcg cat ggt aag ata	384
Leu Phe Arg Ala Ile Arg Val Asp Gly Asn Ser Ser His Gly Lys Ile	
115 120 125	

tct gaa ttt tat gga aag tct gtt gat tca aaa tta gcc tca aga ata 432
 Ser Glu Phe Tyr Gly Lys Ser Val Asp Ser Lys Leu Ala Ser Arg Ile
 130 135 140

ttt gca caa tat cac gaa gat ttg acg agc aaa ttg tca act cag aat 480
 Phe Ala Gln Tyr His Glu Asp Leu Thr Ser Lys Leu Ser Thr Gln Asn
 145 150 155 160

aat ttt att ata tct aaa gat aat taa 507
 Asn Phe Ile Ile Ser Lys Asp Asn
 165

<210> 32

<211> 168

<212> PRT

<213> Moraxella bovis

<400> 32

Met Thr Lys Lys Phe Ala Glu Leu Gly Leu Ile Ala Trp Leu Trp Ser
 1 5 10 15

Asn Ser Asp Met His Lys His Trp Thr Leu Ser Leu Phe Ala Thr Asn
 20 25 30

Val Ile Pro Ala Ile Glu Thr Gly Gln Tyr Val Ile Leu Lys Arg Glu
 35 40 45

Asp Met Pro Val Ala Tyr Cys Ser Trp Ala Lys Leu Ser Leu Glu Asn
 50 55 60

Glu Val Lys Tyr Ile Asn Asp Val Thr Ser Leu Lys Leu Asp Asp Trp
 65 70 75 80

Gln Ser Gly Asp Arg Asn Trp Phe Ile Asp Trp Ile Ala Pro Phe Gly
 85 90 95

Asp Ser Leu Thr Leu Thr Lys His Met Arg Thr Leu Phe Ser Asp Glu
 100 105 110

Leu Phe Arg Ala Ile Arg Val Asp Gly Asn Ser Ser His Gly Lys Ile
 115 120 125

Ser Glu Phe Tyr Gly Lys Ser Val Asp Ser Lys Leu Ala Ser Arg Ile
 130 135 140

Phe Ala Gln Tyr His Glu Asp Leu Thr Ser Lys Leu Ser Thr Gln Asn
 145 150 155 160

Asn Phe Ile Ile Ser Lys Asp Asn
 165

<210> 33

<211> 167

<212> PRT

<213> Pasteurella haemolytica

<400> 33

Met	Asn	Gln	Ser	Tyr	Phe	Asn	Leu	Leu	Gly	Asn	Ile	Thr	Trp	Leu	Trp
1				5					10					15	
Met	Asn	Ser	Ser	Leu	His	Lys	Glu	Trp	Ser	Cys	Glu	Leu	Leu	Ala	Arg
			20					25					30		
Asn	Val	Ile	Pro	Ala	Ile	Glu	Asn	Glu	Gln	Tyr	Met	Leu	Leu	Ile	Asp
		35					40					45			
Asn	Gly	Ile	Pro	Ile	Ala	Tyr	Cys	Ser	Trp	Ala	Asp	Leu	Asn	Leu	Glu
	50					55					60				
Thr	Glu	Val	Lys	Tyr	Ile	Lys	Asp	Ile	Asn	Ser	Leu	Thr	Pro	Glu	Glu
65					70					75				80	
Trp	Gln	Ser	Gly	Asp	Arg	Arg	Trp	Ile	Ile	Asp	Trp	Val	Ala	Pro	Phe
				85					90					95	
Gly	His	Ser	Gln	Leu	Leu	Tyr	Lys	Lys	Met	Cys	Gln	Lys	Tyr	Pro	Asp
			100					105					110		
Met	Ile	Val	Arg	Ser	Ile	Arg	Phe	Tyr	Pro	Lys	Gln	Lys	Glu	Leu	Gly
	115						120					125			
Lys	Ile	Ala	Tyr	Phe	Lys	Gly	Gly	Lys	Leu	Asp	Lys	Lys	Thr	Ala	Lys
	130					135					140				
Lys	Arg	Phe	Asp	Thr	Tyr	Gln	Glu	Glu	Leu	Ala	Thr	Ala	Leu	Lys	Asn
145					150					155				160	
Glu	Phe	Asn	Phe	Ile	Lys	Lys									
				165											

<210> 34

<211> 172

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 34

Met	Ser	Lys	Lys	Ile	Asn	Gly	Phe	Glu	Val	Leu	Gly	Glu	Val	Ala	Trp
1				5					10					15	
Leu	Trp	Ala	Ser	Ser	Pro	Leu	His	Arg	Lys	Trp	Pro	Leu	Ser	Leu	Leu
			20					25					30		
Ala	Ile	Asn	Val	Leu	Pro	Ala	Ile	Glu	Ser	Asn	Gln	Tyr	Val	Leu	Leu
		35					40					45			
Lys	Arg	Asp	Gly	Phe	Pro	Ile	Ala	Phe	Cys	Ser	Trp	Ala	Asn	Leu	Asn
	50					55					60				
Leu	Glu	Asn	Glu	Ile	Lys	Tyr	Leu	Asp	Asp	Val	Ala	Ser	Leu	Val	Ala
65					70					75				80	

Asp Asp Trp Thr Ser Gly Asp Arg Arg Trp Phe Ile Asp Trp Ile Ala
 85 90 95
 Pro Phe Gly Asp Ser Ala Ala Leu Tyr Lys His Met Arg Asp Asn Phe
 100 105 110
 Pro Asn Glu Leu Phe Arg Ala Ile Arg Val Asp Pro Asp Ser Arg Val
 115 120 125
 Gly Lys Ile Ser Glu Phe His Gly Gly Lys Ile Asp Lys Lys Leu Ala
 130 135 140
 Ser Lys Ile Phe Gln Gln Tyr His Phe Glu Leu Met Ser Glu Leu Lys
 145 150 155 160
 Asn Lys Gln Asn Phe Lys Phe Ser Leu Val Asn Ser
 165 170

<210> 35
 <211> 170
 <212> PRT
 <213> Escherichia coli

<400> 35
 Met Asn Arg Asn Asn Pro Leu Glu Val Leu Gly His Val Ser Trp Leu
 1 5 10 15
 Trp Ala Ser Ser Pro Leu His Arg Asn Trp Pro Val Ser Leu Phe Ala
 20 25 30
 Ile Asn Val Leu Pro Ala Ile Arg Ala Asn Gln Tyr Ala Leu Leu Thr
 35 40 45
 Arg Asp Asn Tyr Pro Val Ala Tyr Cys Ser Trp Ala Asn Leu Ser Leu
 50 55 60
 Glu Asn Glu Ile Lys Tyr Leu Asn Asp Val Thr Ser Leu Val Ala Glu
 65 70 75 80
 Asp Trp Thr Ser Gly Asp Arg Lys Trp Phe Ile Val Trp Ile Ala Pro
 85 90 95
 Phe Gly Asp Asn Gly Ala Leu Tyr Lys Tyr Met Arg Lys Lys Phe Pro
 100 105 110
 Asp Glu Leu Phe Arg Ala Ile Arg Val Asp Pro Lys Thr His Val Gly
 115 120 125
 Lys Val Ser Glu Phe His Gly Gly Lys Ile Asp Lys Gln Leu Ala Asn
 130 135 140
 Lys Ile Phe Lys Gln Tyr His His Glu Leu Ile Thr Glu Val Lys Asn
 145 150 155 160
 Lys Ser Asp Phe Asn Phe Ser Leu Thr Gly
 165 170

<210> 36
 <211> 1428
 <212> DNA
 <213> Moraxella bovis

<220>
 <221> CDS
 <222> (1)..(1425)

<400> 36
 atg ttt ata caa gca ctt aaa gat ttt ttt att cgc tat ata acc gtt 48
 Met Phe Ile Gln Ala Leu Lys Asp Phe Phe Ile Arg Tyr Ile Thr Val
 1 5 10 15

tgg cgc aat aca tgg gca gtt cga gac caa cta acc cct cct aag cgt 96
 Trp Arg Asn Thr Trp Ala Val Arg Asp Gln Leu Thr Pro Pro Lys Arg
 20 25 30

act aaa gaa gaa ctc gct ttt ctt cct gca cat cta gaa ctc act gac 144
 Thr Lys Glu Glu Leu Ala Phe Leu Pro Ala His Leu Glu Leu Thr Asp
 35 40 45

aca cct gta tcc aga tct tct aag tgg aca gct aga ata atc atg ata 192
 Thr Pro Val Ser Arg Ser Ser Lys Trp Thr Ala Arg Ile Ile Met Ile
 50 55 60

ttt gtc cta ttt gct ttg cta tgg tct tgg gtt gga cag att gac att 240
 Phe Val Leu Phe Ala Leu Leu Trp Ser Trp Val Gly Gln Ile Asp Ile
 65 70 75 80

gtt gct aca gct tca ggt aaa att tct tca ggt agc cgt agc aag act 288
 Val Ala Thr Ala Ser Gly Lys Ile Ser Ser Gly Ser Arg Ser Lys Thr
 85 90 95

att caa tct ttg gaa aca gcg ata gtt aaa gca gtt tat gta cgt gat 336
 Ile Gln Ser Leu Glu Thr Ala Ile Val Lys Ala Val Tyr Val Arg Asp
 100 105 110

ggt caa aat gtt caa caa ggt gaa ata tta gta gat tta gtg gga atc 384
 Gly Gln Asn Val Gln Gln Gly Glu Ile Leu Val Asp Leu Val Gly Ile
 115 120 125

ggt tca gat agt gat gtt gct cag tcc gag aaa gcc ctt cga gca gcg 432
 Gly Ser Asp Ser Asp Val Ala Gln Ser Glu Lys Ala Leu Arg Ala Ala
 130 135 140

caa tta tct aag cta cgc ctt gaa gca att tta tca gca tta aat cac 480
 Gln Leu Ser Lys Leu Arg Leu Glu Ala Ile Leu Ser Ala Leu Asn His
 145 150 155 160

cgt att aat cct cag att gat gta gca tat gca aag tct tta aat att 528
 Arg Ile Asn Pro Gln Ile Asp Val Ala Tyr Ala Lys Ser Leu Asn Ile
 165 170 175

tca gaa tcg gaa att aat gaa gct caa act tta gcc caa aat caa tat 576
 Ser Glu Ser Glu Ile Asn Glu Ala Gln Thr Leu Ala Gln Asn Gln Tyr
 180 185 190

caa gca tgg tta gca caa gat gaa caa cta aaa tta acc tta aaa gga	624
Gln Ala Trp Leu Ala Gln Asp Glu Gln Leu Lys Leu Thr Leu Lys Gly	
195 200 205	
cat caa gca gaa tta caa tct gct cga tcc caa gaa caa aag ttg gtt	672
His Gln Ala Glu Leu Gln Ser Ala Arg Ser Gln Glu Gln Lys Leu Val	
210 215 220	
tca gtt ggt gca att gaa cat caa aag act gat gat tat cgg agt ctc	720
Ser Val Gly Ala Ile Glu His Gln Lys Thr Asp Asp Tyr Arg Ser Leu	
225 230 235 240	
aaa gca gaa aat ttt ata tct gag cat gct tat cta gaa caa gaa agc	768
Lys Ala Glu Asn Phe Ile Ser Glu His Ala Tyr Leu Glu Gln Glu Ser	
245 250 255	
aaa tta ctt agc aat caa aat gat tta caa agt aca cgt agt cag att	816
Lys Leu Leu Ser Asn Gln Asn Asp Leu Gln Ser Thr Arg Ser Gln Ile	
260 265 270	
caa aaa ata cag gct gca atc atg caa gct gaa cag aac cgt atg tta	864
Gln Lys Ile Gln Ala Ala Ile Met Gln Ala Glu Gln Asn Arg Met Leu	
275 280 285	
tat act caa aat cta aaa cgt gat aca tta gaa tct tta cgc caa acc	912
Tyr Thr Gln Asn Leu Lys Arg Asp Thr Leu Glu Ser Leu Arg Gln Thr	
290 295 300	
aat gaa cag att aat caa tat act ggt caa act aat aaa gct aag cag	960
Asn Glu Gln Ile Asn Gln Tyr Thr Gly Gln Thr Asn Lys Ala Lys Gln	
305 310 315 320	
cga cag aaa ttg ctg agt att aaa tca cct gtt aat ggt act ata caa	1008
Arg Gln Lys Leu Leu Ser Ile Lys Ser Pro Val Asn Gly Thr Ile Gln	
325 330 335	
gag cta aca gct tat act tta ggt gga gtt gta caa gca gca caa aaa	1056
Glu Leu Thr Ala Tyr Thr Leu Gly Gly Val Val Gln Ala Ala Gln Lys	
340 345 350	
att atg gtt gtg gca cct aac gat aat caa gtg gaa gta gag gta tta	1104
Ile Met Val Val Ala Pro Asn Asp Asn Gln Val Glu Val Glu Val Leu	
355 360 365	
gtg cta aat aaa gat atc ggc ttt gta aaa gct ggg cag aat gtt atc	1152
Val Leu Asn Lys Asp Ile Gly Phe Val Lys Ala Gly Gln Asn Val Ile	
370 375 380	
atc aaa atc gag agt ttt cct tat aca cgt tat ggt tat tta aca ggt	1200
Ile Lys Ile Glu Ser Phe Pro Tyr Thr Arg Tyr Gly Tyr Leu Thr Gly	
385 390 395 400	
aaa ata aaa agt att agt cat gat gct ata gaa cat caa cat tta ggt	1248
Lys Ile Lys Ser Ile Ser His Asp Ala Ile Glu His Gln His Leu Gly	
405 410 415	

cta gtg tat act gca ctt gtt tct ctt gat aaa agc aca tta aat ata 1296
 Leu Val Tyr Thr Ala Leu Val Ser Leu Asp Lys Ser Thr Leu Asn Ile
 420 425 430

gat gga gta aca atc aac tta acg cca gga atg aat gtt act gct gaa 1344
 Asp Gly Val Thr Ile Asn Leu Thr Pro Gly Met Asn Val Thr Ala Glu
 435 440 445

att aaa aca ggt aaa cgt cgt gtt ttg gat tat ata tta agt cca ttg 1392
 Ile Lys Thr Gly Lys Arg Arg Val Leu Asp Tyr Ile Leu Ser Pro Leu
 450 455 460

cag aca aaa gtt gat gaa agt ttt cga gaa cgc taa 1428
 Gln Thr Lys Val Asp Glu Ser Phe Arg Glu Arg
 465 470 475

<210> 37

<211> 475

<212> PRT

<213> Moraxella bovis

<400> 37

Met Phe Ile Gln Ala Leu Lys Asp Phe Phe Ile Arg Tyr Ile Thr Val
 1 5 10 15

Trp Arg Asn Thr Trp Ala Val Arg Asp Gln Leu Thr Pro Pro Lys Arg
 20 25 30

Thr Lys Glu Glu Leu Ala Phe Leu Pro Ala His Leu Glu Leu Thr Asp
 35 40 45

Thr Pro Val Ser Arg Ser Ser Lys Trp Thr Ala Arg Ile Ile Met Ile
 50 55 60

Phe Val Leu Phe Ala Leu Leu Trp Ser Trp Val Gly Gln Ile Asp Ile
 65 70 75 80

Val Ala Thr Ala Ser Gly Lys Ile Ser Ser Gly Ser Arg Ser Lys Thr
 85 90 95

Ile Gln Ser Leu Glu Thr Ala Ile Val Lys Ala Val Tyr Val Arg Asp
 100 105 110

Gly Gln Asn Val Gln Gln Gly Glu Ile Leu Val Asp Leu Val Gly Ile
 115 120 125

Gly Ser Asp Ser Asp Val Ala Gln Ser Glu Lys Ala Leu Arg Ala Ala
 130 135 140

Gln Leu Ser Lys Leu Arg Leu Glu Ala Ile Leu Ser Ala Leu Asn His
 145 150 155 160

Arg Ile Asn Pro Gln Ile Asp Val Ala Tyr Ala Lys Ser Leu Asn Ile
 165 170 175

Ser Glu Ser Glu Ile Asn Glu Ala Gln Thr Leu Ala Gln Asn Gln Tyr
 180 185 190

Gln Ala Trp Leu Ala Gln Asp Glu Gln Leu Lys Leu Thr Leu Lys Gly
 195 200 205
 His Gln Ala Glu Leu Gln Ser Ala Arg Ser Gln Glu Gln Lys Leu Val
 210 215 220
 Ser Val Gly Ala Ile Glu His Gln Lys Thr Asp Asp Tyr Arg Ser Leu
 225 230 235 240
 Lys Ala Glu Asn Phe Ile Ser Glu His Ala Tyr Leu Glu Gln Glu Ser
 245 250 255
 Lys Leu Leu Ser Asn Gln Asn Asp Leu Gln Ser Thr Arg Ser Gln Ile
 260 265 270
 Gln Lys Ile Gln Ala Ala Ile Met Gln Ala Glu Gln Asn Arg Met Leu
 275 280 285
 Tyr Thr Gln Asn Leu Lys Arg Asp Thr Leu Glu Ser Leu Arg Gln Thr
 290 295 300
 Asn Glu Gln Ile Asn Gln Tyr Thr Gly Gln Thr Asn Lys Ala Lys Gln
 305 310 315 320
 Arg Gln Lys Leu Leu Ser Ile Lys Ser Pro Val Asn Gly Thr Ile Gln
 325 330 335
 Glu Leu Thr Ala Tyr Thr Leu Gly Gly Val Val Gln Ala Ala Gln Lys
 340 345 350
 Ile Met Val Val Ala Pro Asn Asp Asn Gln Val Glu Val Glu Val Leu
 355 360 365
 Val Leu Asn Lys Asp Ile Gly Phe Val Lys Ala Gly Gln Asn Val Ile
 370 375 380
 Ile Lys Ile Glu Ser Phe Pro Tyr Thr Arg Tyr Gly Tyr Leu Thr Gly
 385 390 395 400
 Lys Ile Lys Ser Ile Ser His Asp Ala Ile Glu His Gln His Leu Gly
 405 410 415
 Leu Val Tyr Thr Ala Leu Val Ser Leu Asp Lys Ser Thr Leu Asn Ile
 420 425 430
 Asp Gly Val Thr Ile Asn Leu Thr Pro Gly Met Asn Val Thr Ala Glu
 435 440 445
 Ile Lys Thr Gly Lys Arg Arg Val Leu Asp Tyr Ile Leu Ser Pro Leu
 450 455 460
 Gln Thr Lys Val Asp Glu Ser Phe Arg Glu Arg
 465 470 475

<210> 38
 <211> 478
 <212> PRT
 <213> *Pasteurella haemolytica*

<400> 38
 Met Lys Ile Trp Leu Ser Gly Ile Tyr Glu Phe Phe Leu Arg Tyr Lys
 1 5 10 15
 Asn Ile Trp Ala Glu Val Trp Lys Ile Arg Lys Glu Leu Asp His Pro
 20 25 30
 Asn Arg Lys Lys Asp Glu Ser Glu Phe Leu Pro Ala His Leu Glu Leu
 35 40 45
 Ile Glu Thr Pro Val Ser Lys Lys Pro Arg Leu Ile Ala Tyr Leu Ile
 50 55 60
 Met Leu Phe Leu Val Val Ala Ile Val Leu Ala Ser Val Ser Lys Val
 65 70 75 80
 Glu Ile Val Ala Thr Ala Pro Gly Lys Leu Thr Phe Ser Gly Arg Ser
 85 90 95
 Lys Glu Ile Lys Pro Ile Glu Asn Ala Ile Val Gln Glu Ile Phe Val
 100 105 110
 Lys Asp Gly Gln Phe Val Glu Lys Gly Gln Leu Leu Val Ser Leu Thr
 115 120 125
 Ala Leu Gly Ser Asp Ala Asp Ile Lys Lys Thr Met Ala Ser Leu Ser
 130 135 140
 Leu Ala Lys Leu Glu Asn Tyr Arg Tyr Gln Thr Leu Leu Thr Ala Ile
 145 150 155 160
 Glu Lys Glu Ser Leu Pro Val Ile Asp Leu Ser Arg Thr Glu Phe Lys
 165 170 175
 Asp Ser Ser Glu Glu Asp Arg Leu Arg Ile Lys His Leu Ile Glu Glu
 180 185 190
 Gln Tyr Thr Thr Trp Gln Lys Gln Lys Thr Gln Lys Thr Leu Ala Tyr
 195 200 205
 Lys Arg Lys Glu Ala Glu Lys Gln Thr Ile Phe Ala Tyr Val Arg Lys
 210 215 220
 Tyr Glu Gly Ala Thr Arg Ile Glu Gln Glu Lys Leu Lys Asp Phe Lys
 225 230 235 240
 Ala Leu Tyr Lys Gln Lys Ser Leu Ser Lys His Glu Leu Leu Ala Gln
 245 250 255
 Glu Asn Lys Leu Ile Glu Ala Gln Asn Ala Val Ala Val Tyr Arg Ser
 260 265 270

Lys Leu Asn Glu Leu Glu Asn Asp Leu Leu Asn Val Lys Glu Glu Leu
275 280 285

Glu Leu Ile Thr Gln Phe Phe Lys Ser Asp Val Leu Glu Lys Leu Lys
290 295 300

Gln His Ile Glu Asn Glu Arg Gln Leu Arg Leu Glu Leu Glu Lys Asn
305 310 315 320

Asn Gln Arg Arg Gln Ala Ser Met Ile Arg Ala Pro Val Ser Gly Thr
325 330 335

Val Gln Gln Leu Lys Ile His Thr Ile Gly Gly Val Val Thr Thr Ala
340 345 350

Glu Thr Leu Met Ile Ile Val Pro Glu Asp Asp Val Leu Glu Ala Thr
355 360 365

Ala Leu Val Pro Asn Lys Asp Ile Gly Phe Val Ala Ala Gly Gln Glu
370 375 380

Val Ile Ile Lys Val Glu Thr Phe Pro Tyr Thr Arg Tyr Gly Tyr Leu
385 390 395 400

Thr Gly Arg Ile Lys His Ile Ser Pro Asp Ala Ile Glu Gln Pro Asn
405 410 415

Val Gly Leu Val Phe Asn Ala Thr Ile Ala Ile Asp Arg Lys Asn Leu
420 425 430

Thr Ser Pro Asp Gly Arg Lys Ile Asp Leu Ser Ser Gly Met Thr Ile
435 440 445

Thr Ala Glu Ile Lys Thr Gly Glu Arg Ser Val Met Ser Tyr Leu Leu
450 455 460

Ser Pro Leu Glu Glu Ser Val Thr Glu Ser Leu Arg Glu Arg
465 470 475

<210> 39

<211> 478

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 39

Met Lys Thr Trp Leu Met Gly Leu Tyr Glu Phe Phe Gln Arg Tyr Lys
1 5 10 15

Thr Val Trp Thr Glu Ile Trp Lys Ile Arg His Gln Leu Asp Thr Pro
20 25 30

Asp Arg Glu Lys Asp Glu Asn Glu Phe Leu Pro Ala His Leu Glu Leu
35 40 45

Ile Glu Thr Pro Val Ser Lys Lys Pro Arg Leu Ile Ala Tyr Leu Ile
50 55 60

Met	Leu	Phe	Leu	Phe	Leu	Ala	Leu	Val	Ile	Ser	Ile	Val	Ser	His	Val	65	70	75	80
Glu	Ile	Val	Ala	Thr	Ala	Thr	Gly	Lys	Leu	Ala	Phe	Ser	Asp	Arg	Ser	85	90	95	
Lys	Glu	Ile	Lys	Pro	Ile	Glu	Asn	Ala	Leu	Val	Lys	Glu	Ile	Phe	Val	100	105	110	
Gln	Asp	Gly	Gln	Phe	Val	Glu	Lys	Asp	Gln	Leu	Leu	Leu	His	Leu	Thr	115	120	125	
Ala	Leu	Gly	Ala	Asp	Ala	Asp	Gln	Gln	Lys	Thr	Lys	Ser	Ser	Leu	Ser	130	135	140	
Leu	Thr	Lys	Leu	Glu	Arg	Tyr	Arg	Tyr	Glu	Ile	Leu	Leu	Glu	Ala	Val	145	150	155	160
Ala	Ala	Asp	Arg	Leu	Pro	Leu	Ile	Glu	Leu	Thr	Lys	Asp	Glu	Phe	Lys	165	170	175	
His	Ala	Thr	Glu	Glu	Asp	Lys	Thr	Arg	Ile	Arg	Tyr	Leu	Ile	Thr	Glu	180	185	190	
Gln	Phe	Glu	Ala	Trp	Gln	Lys	Gln	Lys	Tyr	Gln	Lys	Glu	Leu	Ala	Leu	195	200	205	
Gln	Arg	Arg	Glu	Ala	Glu	Lys	Gln	Thr	Val	Leu	Ala	Asn	Ile	Arg	Lys	210	215	220	
Tyr	Glu	Gly	Ile	Ser	Arg	Val	Glu	Asn	Glu	Arg	Leu	Lys	Asp	Leu	Lys	225	230	235	240
Lys	Leu	Phe	Asn	Ser	Lys	Ser	Thr	Ser	Lys	His	Asp	Val	Leu	Thr	Gln	245	250	255	
Glu	Asn	Arg	His	Ile	Glu	Ala	Val	Asn	Glu	Leu	Ala	Val	Tyr	Lys	Ser	260	265	270	
Arg	Leu	Asn	Glu	Val	Glu	Ser	Asp	Leu	Arg	Gln	Ala	Lys	Glu	Glu	Ile	275	280	285	
His	Leu	Ile	Thr	Gln	Leu	Phe	Arg	Ala	Asp	Ile	Leu	Glu	Lys	Leu	Lys	290	295	300	
Gln	Asn	Val	Glu	Ala	Glu	Lys	Gln	Leu	Ser	Leu	Glu	Leu	Glu	Lys	Asn	305	310	315	320
Glu	Gln	Arg	Gln	Ile	Ala	Ser	Val	Ile	Arg	Ala	Pro	Val	Ser	Gly	Thr	325	330	335	
Val	Gln	Gln	Leu	Lys	Thr	His	Thr	Val	Gly	Gly	Val	Val	Thr	Thr	Ala	340	345	350	
Glu	Thr	Leu	Met	Val	Ile	Ala	Pro	Glu	Asp	Asp	Val	Leu	Glu	Val	Thr	355	360	365	

Ala Leu Ile Gln Asn Lys Asp Ile Gly Phe Ile Glu Val Gly Gln Asp
370 375 380

Ala Val Ile Lys Val Glu Thr Phe Pro Tyr Thr Arg Tyr Gly Tyr Leu
385 390 395 400

Met Gly Lys Val Lys Asn Ile Thr Leu Glu Ala Ile Glu His Pro Gln
405 410 415

Leu Gly Leu Val Phe Asn Ser Ile Ile Ser Ile Asp Arg Lys Thr Leu
420 425 430

Ser Gly Lys Asp Gly Lys Glu Ile Glu Leu Gly Ser Gly Met Ser Val
435 440 445

Thr Ala Glu Ile Lys Thr Gly Glu Arg Ser Val Ile Ser Tyr Leu Leu
450 455 460

Ser Pro Leu Glu Glu Ser Val Ser Glu Ser Leu Arg Glu Arg
465 470 475

<210> 40

<211> 478

<212> PRT

<213> Escherichia coli

<400> 40

Met Lys Thr Trp Leu Met Gly Phe Ser Glu Phe Leu Leu Arg Tyr Lys
1 5 10 15

Leu Val Trp Ser Glu Thr Trp Lys Ile Arg Lys Gln Leu Asp Thr Pro
20 25 30

Val Arg Glu Lys Asp Glu Asn Glu Phe Leu Pro Ala His Leu Glu Leu
35 40 45

Ile Glu Thr Pro Val Ser Arg Arg Pro Arg Leu Val Ala Tyr Phe Ile
50 55 60

Met Gly Phe Leu Val Ile Ala Phe Ile Leu Ser Val Leu Gly Gln Val
65 70 75 80

Glu Ile Val Ala Thr Ala Asn Gly Lys Leu Thr Leu Ser Gly Arg Ser
85 90 95

Lys Glu Ile Lys Pro Ile Glu Asn Ser Ile Val Lys Glu Ile Ile Val
100 105 110

Lys Glu Gly Glu Ser Val Arg Lys Gly Asp Val Leu Leu Lys Leu Thr
115 120 125

Ala Leu Gly Ala Glu Ala Asp Thr Leu Lys Thr Gln Ser Ser Leu Leu
130 135 140

Gln Ala Arg Leu Glu Gln Ile Arg Tyr Gln Ile Leu Ser Arg Ser Ile
145 150 155 160

Glu	Leu	Asn	Lys	Leu	Pro	Glu	Leu	Lys	Leu	Pro	Asp	Glu	Pro	Tyr	Phe	165	170	175
Gln	Asn	Val	Ser	Glu	Glu	Glu	Val	Leu	Arg	Leu	Thr	Ser	Leu	Ile	Lys	180	185	190
Glu	Gln	Phe	Ser	Thr	Trp	Gln	Asn	Gln	Lys	Tyr	Gln	Lys	Glu	Leu	Asn	195	200	205
Leu	Asp	Lys	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ile	Leu	Ala	Arg	Ile	Asn	210	215	220
Arg	Tyr	Glu	Asn	Val	Ser	Arg	Val	Glu	Lys	Ser	Arg	Leu	Asp	Asp	Phe	225	230	235
Arg	Ser	Leu	Leu	His	Lys	Gln	Ala	Ile	Ala	Lys	His	Ala	Val	Leu	Glu	245	250	255
Gln	Glu	Asn	Lys	Tyr	Val	Glu	Ala	Ala	Asn	Glu	Leu	Arg	Val	Tyr	Lys	260	265	270
Ser	Gln	Leu	Glu	Gln	Ile	Glu	Ser	Glu	Ile	Leu	Ser	Ala	Lys	Glu	Glu	275	280	285
Tyr	Gln	Leu	Val	Thr	Gln	Leu	Phe	Lys	Asn	Glu	Ile	Leu	Asp	Lys	Leu	290	295	300
Arg	Gln	Thr	Thr	Asp	Ser	Ile	Glu	Leu	Leu	Thr	Leu	Glu	Leu	Glu	Lys	305	310	315
Asn	Glu	Glu	Arg	Gln	Gln	Ala	Ser	Val	Ile	Arg	Ala	Pro	Val	Ser	Gly	325	330	335
Lys	Val	Gln	Gln	Leu	Lys	Val	His	Thr	Glu	Gly	Gly	Val	Val	Thr	Thr	340	345	350
Ala	Glu	Thr	Leu	Met	Val	Ile	Val	Pro	Glu	Asp	Asp	Thr	Leu	Glu	Val	355	360	365
Thr	Ala	Leu	Val	Gln	Asn	Lys	Asp	Ile	Gly	Phe	Ile	Asn	Val	Gly	Gln	370	375	380
Asn	Ala	Ile	Ile	Lys	Val	Glu	Ala	Phe	Pro	Tyr	Thr	Arg	Tyr	Gly	Tyr	385	390	395
Leu	Val	Gly	Lys	Val	Lys	Asn	Ile	Asn	Leu	Asp	Ala	Ile	Glu	Asp	Gln	405	410	415
Lys	Leu	Gly	Leu	Val	Phe	Asn	Val	Ile	Val	Ser	Val	Glu	Glu	Asn	Asp	420	425	430
Leu	Ser	Thr	Gly	Asn	Lys	His	Ile	Pro	Leu	Ser	Ser	Gly	Met	Ala	Val	435	440	445
Thr	Ala	Glu	Ile	Lys	Thr	Gly	Met	Arg	Ser	Val	Ile	Ser	Tyr	Leu	Leu	450	455	460

Ser Pro Leu Glu Glu Ser Val Thr Glu Ser Leu His Glu Arg
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<223> Description of Artificial Sequence: Primer

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